STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10 563 503*
Source: *TFWP*
Date Processed by STIC: *1-13-06*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10 563/503

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13__✓__Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

RAW SEQUENCE LISTING   DATE: 01/13/2006
PATENT APPLICATION: US/10/563,503   TIME: 12:10:37

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\01132006\J563503.raw

```
    5 <110> APPLICANT: Stordeur, Patrick
    6         Goldman, Michel
   10 <120> TITLE OF INVENTION: Device, kit and method for pulsing biological samples with
an agent and
   11         stabilising the sample so pulsed
   15 <130> FILE REFERENCE: DECLE35.005APC
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/563,503
C--> 20 <141> CURRENT FILING DATE: 2006-01-04
   22 <150> PRIOR APPLICATION NUMBER: PCT/EP03/07453
   24 <151> PRIOR FILING DATE: 2003-07-10
   28 <160> NUMBER OF SEQ ID NOS: 10
   32 <170> SOFTWARE: PatentIn version 3.1
   36 <210> SEQ ID NO: 1
   38 <211> LENGTH: 22
   40 <212> TYPE: DNA
   42 <213> ORGANISM: Homo sapiens
   46 <400> SEQUENCE: 1
   47 ctcaccagga tgctcacatt ta                                          22
   48 <210> SEQ ID NO: 2
   50 <211> LENGTH: 24
   52 <212> TYPE: DNA
   54 <213> ORGANISM: Homo sapiens
   58 <400> SEQUENCE: 2
   59 tccagaggtt tgagttcttc ttct                                        24
   60 <210> SEQ ID NO: 3
   62 <211> LENGTH: 25
   64 <212> TYPE: DNA
   66 <213> ORGANISM: Homo sapiens
   70 <220> FEATURE:
   72 <221> NAME/KEY: misc_feature
   74 <222> LOCATION: (1)..(1)
   76 <223> OTHER INFORMATION: N = 6Fam
   79 <220> FEATURE:
   81 <221> NAME/KEY: misc_feature
   83 <222> LOCATION: (25)..(25)
   85 <223> OTHER INFORMATION: N = Tamra-p
   88 <400> SEQUENCE: 3
W--> 89 ntgcccaaga aggccacaga actgn                                      25
   90 <210> SEQ ID NO: 4
   92 <211> LENGTH: 21
   94 <212> TYPE: DNA
   96 <213> ORGANISM: Homo sapiens
  100 <400> SEQUENCE: 4
  101 actttgaaca gcctcacaga g                                           21
```

Does Not Comply
Corrected Diskette Needed
_(Pg. 1-2)_

Invalid response

← pls see item #13 on error summary sheet.

RAW SEQUENCE LISTING   DATE: 01/13/2006
PATENT APPLICATION: US/10/563,503   TIME: 12:10:37

          Input Set : A:\pto.da.txt
          Output Set: N:\CRF4\01132006\J563503.raw

```
102 <210> SEQ ID NO: 5
104 <211> LENGTH: 20
106 <212> TYPE: DNA
108 <213> ORGANISM: Homo sapiens
112 <400> SEQUENCE: 5
113 ttggaggcag caaagatgtc                                           20
114 <210> SEQ ID NO: 6
116 <211> LENGTH: 23
118 <212> TYPE: DNA
120 <213> ORGANISM: Homo sapiens
124 <220> FEATURE:
126 <221> NAME/KEY: misc_feature
128 <222> LOCATION: (1)..(1)
130 <223> OTHER INFORMATION: N -(6Fam)
133 <220> FEATURE:
135 <221> NAME/KEY: misc_feature
137 <222> LOCATION: (23)..(23)
139 <223> OTHER INFORMATION: N =(Tamra-p)
142 <400> SEQUENCE: 6
143 nctgtgcacc gagttgaccg tan                                       23
144 <210> SEQ ID NO: 7
146 <211> LENGTH: 22
148 <212> TYPE: DNA
150 <213> ORGANISM: Homo sapiens
154 <400> SEQUENCE: 7
155 tgtcacaaac agtgcaccta ct
156 <210> SEQ ID NO: 8
158 <211> LENGTH: 26
160 <212> TYPE: DNA
162 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 8
167 agttacaata ggtagcaaac cataca                                    26
168 <210> SEQ ID NO: 9
170 <211> LENGTH: 21
172 <212> TYPE: DNA
174 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 9
179 taattgcctc acattgtcac t                                         21
180 <210> SEQ ID NO: 10
182 <211> LENGTH: 21
184 <212> TYPE: DNA
186 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 10
191 attcagctcg aacactttga a                                         21
```

W--> 143 (handwritten marginalia)

Invalid response

← See item #13 on
error summary
sheet.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/13/2006
PATENT APPLICATION: US/10/563,503   TIME: 12:10:38

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\01132006\J563503.raw**

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1,25
Seq#:6; N Pos. 1,23

VERIFICATION SUMMARY   DATE: 01/13/2006
PATENT APPLICATION: US/10/563,503   TIME: 12:10:38

        Input Set : **A:\pto.da.txt**
        Output Set: **N:\CRF4\01132006\J563503.raw**

L:19 M:270 C: Current Application Number differs, Replaced Application Number
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0